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OIPÉ

RAW SEQUENCE LISTING

DATE: 11/06/2001

PATENT APPLICATION: US/09/976,674

TIME: 15:12:49

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Output Set: N:\CRF3\11062001\I976674.raw

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3 <110> APPLICANT: Qi, Steve
 4 Akinsanya, Karen
 5 Riviere, Pierre
 6 Junien, Jean-Louis
 8 <120> TITLE OF INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO DPPIV
 10 <130> FILE REFERENCE: 70669
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/976,674
 C--> 12 <141> CURRENT FILING DATE: 2001-10-12
 12 <150> PRIOR APPLICATION NUMBER: US 60/240,117
 13 <151> PRIOR FILING DATE: 2000-10-12
 15 <160> NUMBER OF SEQ ID NOS: 61
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 882
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
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 31 20 25 30
 34 Glu Pro Phe Tyr Val Glu Arg Tyr Ser Trp Ser Gln Leu Lys Lys Leu
 35 35 40 45
 38 Leu Ala Asp Thr Arg Lys Tyr His Gly Tyr Met Met Ala Lys Ala Pro
 39 50 55 60
 42 His Asp Phe Met Phe Val Lys Arg Asn Asp Pro Asp Gly Pro His Ser
 43 65 70 75 80
 46 Asp Arg Ile Tyr Tyr Leu Ala Met Ser Gly Glu Asn Arg Glu Asn Thr
 47 85 90 95
 50 Leu Phe Tyr Ser Glu Ile Pro Lys Thr Ile Asn Arg Ala Ala Val Leu
 51 100 105 110
 54 Met Leu Ser Trp Lys Pro Leu Leu Asp Leu Phe Gln Ala Thr Leu Asp
 55 115 120 125
 58 Tyr Gly Met Tyr Ser Arg Glu Glu Glu Leu Leu Arg Glu Arg Lys Arg
 59 130 135 140
 62 Ile Gly Thr Val Gly Ile Ala Ser Tyr Asp Tyr His Gln Gly Ser Gly
 63 145 150 155 160
 66 Thr Phe Leu Phe Gln Ala Gly Ser Gly Ile Tyr His Val Lys Asp Gly
 67 165 170 175
 70 Gly Pro Gln Gly Phe Thr Gln Gln Pro Leu Arg Pro Asn Leu Val Glu
 71 180 185 190
 74 Thr Ser Cys Pro Asn Ile Arg Met Asp Pro Lys Leu Cys Pro Ala Asp
 75 195 200 205
 78 Pro Asp Trp Ile Ala Phe Ile His Ser Asn Asp Ile Trp Ile Ser Asn
 79 210 215 220
 82 Ile Val Thr Arg Glu Glu Arg Arg Leu Thr Tyr Val His Asn Glu Leu
 83 225 230 235 240

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86 Ala Asn Met Glu Glu Asp Ala Arg Ser Ala Gly Val Ala Thr Phe Val
87           245           250           255
90 Leu Gln Glu Glu Phe Asp Arg Tyr Ser Gly Tyr Trp Trp Cys Pro Lys
91           260           265           270
94 Ala Glu Thr Thr Pro Ser Gly Gly Lys Ile Leu Arg Ile Leu Tyr Glu
95           275           280           285
98 Glu Asn Asp Glu Ser Glu Val Glu Ile Ile His Val Thr Ser Pro Met
99           290           295           300
102 Leu Glu Thr Arg Arg Ala Asp Ser Phe Arg Tyr Pro Lys Thr Gly Thr
103 305           310           315           320
106 Ala Asn Pro Lys Val Thr Phe Lys Met Ser Glu Ile Met Ile Asp Ala
107           325           330           335
110 Glu Gly Arg Ile Ile Asp Val Ile Asp Lys Glu Leu Ile Gln Pro Phe
111           340           345           350
114 Glu Ile Leu Phe Glu Gly Val Glu Tyr Ile Ala Arg Ala Gly Trp Thr
115           355           360           365
118 Pro Glu Gly Lys Tyr Ala Trp Ser Ile Leu Leu Asp Arg Ser Gln Thr
119           370           375           380
122 Arg Leu Gln Ile Val Leu Ile Ser Pro Glu Leu Phe Ile Pro Val Glu
123 385           390           395           400
126 Asp Asp Val Met Glu Arg Gln Arg Leu Ile Glu Ser Val Pro Asp Ser
127           405           410           415
130 Val Thr Pro Leu Ile Ile Tyr Glu Glu Thr Thr Asp Ile Trp Ile Asn
131           420           425           430
134 Ile His Asp Ile Phe His Val Phe Pro Gln Ser His Glu Glu Glu Ile
135           435           440           445
138 Glu Phe Ile Phe Ala Ser Glu Cys Lys Thr Gly Phe Arg His Leu Tyr
139           450           455           460
142 Lys Ile Thr Ser Ile Leu Lys Glu Ser Lys Tyr Lys Arg Ser Ser Gly
143 465           470           475           480
146 Gly Leu Pro Ala Pro Ser Asp Phe Lys Cys Pro Ile Lys Glu Glu Ile
147           485           490           495
150 Ala Ile Thr Ser Gly Glu Trp Glu Val Leu Gly Arg His Gly Ser Asn
151           500           505           510
154 Ile Gln Val Asp Glu Val Arg Arg Leu Val Tyr Phe Glu Gly Thr Lys
155           515           520           525
158 Asp Ser Pro Leu Glu His His Leu Tyr Val Val Ser Tyr Val Asn Pro
159           530           535           540
162 Gly Glu Val Thr Arg Leu Thr Asp Arg Gly Tyr Ser His Ser Cys Cys
163 545           550           555           560
166 Ile Ser Gln His Cys Asp Phe Phe Ile Ser Lys Tyr Ser Asn Gln Lys
167           565           570           575
170 Asn Pro His Cys Val Ser Leu Tyr Lys Leu Ser Ser Pro Glu Asp Asp
171           580           585           590
174 Pro Thr Cys Lys Thr Lys Glu Phe Trp Ala Thr Ile Leu Asp Ser Ala
175           595           600           605
178 Gly Pro Leu Pro Asp Tyr Thr Pro Pro Glu Ile Phe Ser Phe Glu Ser
179           610           615           620
182 Thr Thr Gly Phe Thr Leu Tyr Gly Met Leu Tyr Lys Pro His Asp Leu

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183 625          630          635          640
186 Gln Pro Gly Lys Lys Tyr Pro Thr Val Leu Phe Ile Tyr Gly Gly Pro
187          645          650          655
190 Gln Val Gln Leu Val Asn Asn Arg Phe Lys Gly Val Lys Tyr Phe Arg
191          660          665          670
194 Leu Asn Thr Leu Ala Ser Leu Gly Tyr Val Val Val Val Ile Asp Asn
195          675          680          685
198 Arg Gly Ser Cys His Arg Gly Leu Lys Phe Glu Gly Ala Phe Lys Tyr
199          690          695          700
202 Lys Met Gly Gln Ile Glu Ile Asp Asp Gln Val Glu Gly Leu Gln Tyr
203 705          710          715          720
206 Leu Ala Ser Arg Tyr Asp Phe Ile Asp Leu Asp Arg Val Gly Ile His
207          725          730          735
210 Gly Trp Ser Tyr Gly Gly Tyr Leu Ser Leu Met Ala Leu Met Gln Arg
211          740          745          750
214 Ser Asp Ile Phe Arg Val Ala Ile Ala Gly Ala Pro Val Thr Leu Trp
215          755          760          765
218 Ile Phe Tyr Asp Thr Gly Tyr Thr Glu Arg Tyr Met Gly His Pro Asp
219          770          775          780
222 Gln Asn Glu Gln Gly Tyr Tyr Leu Gly Ser Val Ala Met Gln Ala Glu
223 785          790          795          800
226 Lys Phe Pro Ser Glu Pro Asn Arg Leu Leu Leu Leu His Gly Phe Leu
227          805          810          815
230 Asp Glu Asn Val His Phe Ala His Thr Ser Ile Leu Leu Ser Phe Leu
231          820          825          830
234 Val Arg Ala Gly Lys Pro Tyr Asp Leu Gln Ile Tyr Pro Gln Glu Arg
235          835          840          845
238 His Ser Ile Arg Val Pro Glu Ser Gly Glu His Tyr Glu Leu His Leu
239          850          855          860
242 Leu His Tyr Leu Gln Glu Asn Leu Gly Ser Arg Ile Ala Ala Leu Lys
243 865          870          875          880
246 Val Ile

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250 <210> SEQ ID NO: 2

251 <211> LENGTH: 2671

252 <212> TYPE: DNA

253 <213> ORGANISM: Homo sapiens

255 <400> SEQUENCE: 2

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258 ggactgtgag gagaatattg aatcacagga tcggcctaaa ttggagcctt tttatgttga      120
260 gcggtattoc tggagtcagc ttaaaaagct gcttgccgat accagaaaat atcatggcta      180
262 catgatggct aaggcaccac atgatttcat gtttgtgaag aggaatgata cagatggacc      240
264 tcattcagac agaattctatt accttgccat gtctgggtgag aacagagaaa atacactgtt      300
266 ttattctgaa attcccaaaa ctatcaatag agcagcagtc ttaatgctct cttggaagcc      360
268 tcttttggat ctttttcagg caacactgga ctatggaatg tattctcgag aagaagaact      420
270 attaagagaa agaaaacgca ttggaacagt cggaattgct tcttacgatt atcaccaagg      480
272 aagtggaaca tttctgtttc aagccggtag tggaatttat cacgtaaaag atggagggcc      540
274 acaaggattt acgcaacaac ctttaaggcc caatctagtg gaaactagtt gtcccaacat      600
276 acggatggat ccaaaattat gccctgctga tccagactgg attgctttta tacatagcaa      660
278 cgatatttgg atatctaaca tcgtaaccag agaagaaagg agactcactt atgtgcacaa      720

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280 tgagctagcc aacatggaag aagatgccag atcagctgga gtcgctacct ttgtttctcca 780
282 agaagaattht gatagatatt ctggctattg gtggtgtcca aaagctgaaa caactcccag 840
284 tgggtggtaaa attcttagaa ttctatatga agaaaatgat gaatctgagg tggaaattat 900
286 tcatgtttaca tcccctatgt tggaaacaag gagggcagat tcattccggt atcctaaaac 960
288 aggtacagca aatcctaaag tcacttttaa gatgtcagaa ataatgattg atgctgaagg 1020
290 aaggatcata gatgtcatag ataaggaact aattcaacct tttgagattc tatttgaagg 1080
292 agttgaatat attgccagag ctggatggac tcctgaggga aaatatgctt ggtccatcct 1140
294 actagatcgc tcccagactc gcctgcagat agtgttgatc tcacctgaat tatttatccc 1200
296 agtagaagat gatgttatgg aaaggcagag actcattgag tcagtgcctg attctgtgac 1260
298 gccactaatt atctatgaag aaacaacaga catctggata aatatccatg acatctttca 1320
300 tgtttttccc caaagtcacg aagaggaaat tgagtttatt tttgcctctg aatgcaaaac 1380
302 aggtttccgt catttataca aaattacatc tattttaaag gaaagcaaat ataaacgac 1440
304 cagtgggtgg ctgcctgctc caagtgattt caagtgtcct atcaaagagg agatagcaat 1500
306 taccagtggg gaatgggaag ttcttgccg gcattggatc aatatccaag ttgatgaagt 1560
308 cagaaggctg gtatattht aaggcaccaa agactcccct ttagagcacc acctgtacgt 1620
310 agtcagttac gtaaactcctg gagaggtgac aaggctgact gaccgtggct actcacattc 1680
312 ttgctgcacc agtcagcact gtgacttctt tataagtaag tatagtaacc agaagaatcc 1740
314 aactgtgtg tccctttaca agctatcaag tcctgaagat gacccaactt gcaaaacaaa 1800
316 ggaattttgg gccaccattt tggattcagc aggtcctctt cctgactata ctctccaga 1860
318 aattttctct tttgaaagta ctactggatt tacattgtat gggatgctct acaagcctca 1920
320 tgactctacg cctggaaaga aatatcctac tgtgctgttc atatatggg gtcctcagg 1980
322 gcagttggg aataatcgat ttaaaggagt caagtatttc cgcttgaata ccctagcctc 2040
324 tctaggttat gtggtttag tgatagacaa caggggatcc tgtcaccgag ggcttaaatt 2100
326 tgaaggcgcc tttaaataa aaatgggtca aatagaaatt gacgatcagg tggaggact 2160
328 ccaatatcta gcttctcgat atgatttcat tgacttagat cgtgtgggca tccacggctg 2220
330 gtccatgga ggatacctct ccctgatggc attaatgcag aggtcagata tcttcagggt 2280
332 tgctattgct ggggccccag tcactctgtg gatcttctat gatacaggat acacggaacg 2340
334 ttatatgggt caccctgacc agaatgaaca gggctattac ttaggatctg tggccatgca 2400
336 agcagaaaag tcccctctg aaccaaactg tttactgctc ttacatgggt tcctggatga 2460
338 gaatgtccat tttgcacata ccagtatatt actgagtttt ttagtgaggg ctggaaagcc 2520
340 atatgattta cagatctatc ctccaggag agacagcata agagttcctg aatcgggaga 2580
342 acattatgaa ctgcatcttt tgcactacct tcaagaaaac cttggatcac gtattgctgc 2640
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347 <210> SEQ ID NO: 3

348 <211> LENGTH: 863

349 <212> TYPE: PRT

350 <213> ORGANISM: Homo sapiens

352 <400> SEQUENCE: 3

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358 Thr Asp Asp Pro Ala Ala Arg Phe Gln Val Gln Lys His Ser Trp Asp
359 20 25 30
362 Gly Leu Arg Ser Ile Ile His Gly Ser Arg Lys Tyr Ser Gly Leu Ile
363 35 40 45
366 Val Asn Lys Ala Pro His Asp Phe Gln Phe Val Gln Lys Thr Asp Glu
367 50 55 60
370 Ser Gly Pro His Ser His Arg Leu Tyr Tyr Leu Gly Met Pro Tyr Gly
371 65 70 75 80
374 Ser Arg Glu Asn Ser Leu Leu Tyr Ser Glu Ile Pro Lys Lys Val Arg

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375          85          90          95
378 Lys Glu Ala Leu Leu Leu Ser Trp Lys Gln Met Leu Asp His Phe
379          100          105          110
382 Gln Ala Thr Pro His His Gly Val Tyr Ser Arg Glu Glu Glu Leu Leu
383          115          120          125
386 Arg Glu Arg Lys Arg Leu Gly Val Phe Gly Ile Thr Ser Tyr Asp Phe
387          130          135          140
390 His Ser Glu Ser Gly Leu Phe Leu Phe Gln Ala Ser Asn Ser Leu Phe
391 145          150          155          160
394 His Cys Arg Asp Gly Gly Lys Asn Gly Phe Met Val Ser Pro Met Lys
395          165          170          175
398 Pro Leu Glu Ile Lys Thr Gln Cys Ser Gly Pro Arg Met Asp Pro Lys
399          180          185          190
402 Ile Cys Pro Ala Asp Pro Ala Phe Phe Ser Phe Ile Asn Asn Ser Asp
403          195          200          205
406 Leu Trp Val Ala Asn Ile Glu Thr Gly Glu Glu Arg Arg Leu Thr Phe
407          210          215          220
410 Cys His Gln Gly Leu Ser Asn Val Leu Asp Asp Pro Lys Ser Ala Gly
411 225          230          235          240
414 Val Ala Thr Phe Val Ile Gln Glu Glu Phe Asp Arg Phe Thr Gly Tyr
415          245          250          255
418 Trp Trp Cys Pro Thr Ala Ser Trp Glu Gly Ser Glu Gly Leu Lys Thr
419          260          265          270
422 Leu Arg Ile Leu Tyr Glu Glu Val Asp Glu Ser Glu Val Glu Val Ile
423          275          280          285
426 His Val Pro Ser Pro Ala Leu Glu Glu Arg Lys Thr Asp Ser Tyr Arg
427          290          295          300
430 Tyr Pro Arg Thr Gly Ser Lys Asn Pro Lys Ile Ala Leu Lys Leu Ala
431 305          310          315          320
434 Glu Phe Gln Thr Asp Ser Gln Gly Lys Ile Val Ser Thr Gln Glu Lys
435          325          330          335
438 Glu Leu Val Gln Pro Phe Ser Ser Leu Phe Pro Lys Val Glu Tyr Ile
439          340          345          350
442 Ala Arg Ala Gly Trp Thr Arg Asp Gly Lys Tyr Ala Trp Ala Met Phe
443          355          360          365
446 Leu Asp Arg Pro Gln Gln Trp Leu Gln Leu Val Leu Leu Pro Pro Ala
447          370          375          380
450 Leu Phe Ile Pro Ser Thr Glu Asn Glu Glu Gln Arg Leu Ala Ser Ala
451 385          390          395          400
454 Arg Ala Val Pro Arg Asn Val Gln Pro Tyr Val Val Tyr Glu Glu Val
455          405          410          415
458 Thr Asn Val Trp Ile Asn Val His Asp Ile Phe Tyr Pro Phe Pro Gln
459          420          425          430
462 Ser Glu Gly Glu Asp Glu Leu Cys Phe Leu Arg Ala Asn Glu Cys Lys
463          435          440          445
466 Thr Gly Phe Cys His Leu Tyr Lys Val Thr Ala Val Leu Lys Ser Gln
467          450          455          460
470 Gly Tyr Asp Trp Ser Glu Pro Phe Ser Pro Gly Glu Asp Glu Phe Lys
471 465          470          475          480

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VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date